65. (New) A method to acquire a monoclonal antibody or scFv/Fab fragments thereof against a target structure comprising the steps of:

(A) exposing a first mounted tissue to an initial monoclonal antibody or scFv/Fab fragment library;

(B) eluting directly from the first mounted tissue unbound elements, wherein the unbound elements comprise a first enriched library;

(C) recovering a second enriched library comprising bound elements by cleaving the bound elements from the first mounted tissue such that the monoclonal antibody or scFv/Fab fragment thereof remains bound to the first mounted tissue;

(D) amplifying either the first or second enriched libraries;

(E) repeating steps (A) to (B) to negatively enrich the unbound elements of the first enriched library or repeating steps (A) to (C) to positively enrich the bound elements of the second enriched library;

(F) exposing the negatively or positively enriched elements of step (E) to a second mounted tissue;

(G) eluting directly from the second mounted tissue unbound elements from the second mounted tissue, wherein the unbound elements comprise a third enriched library;

(H) recovering a fourth enriched library comprising second tissue section bound elements by cleaving the bound elements from the second mounted tissue such that the monoclonal antibody or scFv/Fab fragment thereof remains bound to the second mounted tissue; and

(I) isolating an individual element from either the third or fourth enriched libraries, wherein the individual element is the monoclonal antibody or the scFv/Fab fragment thereof.

66. (New) The method of claim 65 further comprising repeating steps (A) to (I).

67. (New) The method of claim 65 further comprising repeating steps (F) to (I).

68. (New) The method of claim 65 further comprising repeating steps (A) to (E).

69. (New) The method of claim 65 further comprising the step of characterizing a binding pattern of the individual element against the target structure of the first and second mounted tissues.

70. (New) The method of claim 69, wherein the binding pattern is specific for a physiological process.

71. (New) The method of claim 70, wherein the physiological process is a pathological process, cell development and differentiation, tissue development and differentiation, a drug response, or a naturally occurring degradation process.

72. (New) The method of claim 71, wherein the pathological process is inflammation, a secondary tumor deposit or tumor vasculature.

73. (New) The method of claim 65, wherein the target structure of the tissue sections is extracellular or intracellular.

74. (New) The method of claim 73, wherein the intracellular target structure is located intranuclear of a nuclear membrane.

75. (New) The method of claim 73, wherein the extracellular target structure is on the cell surface or a molecule released from a cell.

76. (New) The method of claim 75, wherein the cell is a tumor cell.

77. (New) The method of claim 75, wherein the molecule is released actively or passively.

78. (New) The method of claim 69, wherein the target structure is a ligand, a receptor, an adhesion molecule, a matrix associated molecule or a combination thereof.

79. (New) The method of claim 69, wherein the target structure is a protein, a carbohydrate, a nucleic acid or a lipid.

80. (New) The method of claim 65, wherein the first or second mounted tissue is a frozen tissue section or a fixed tissue section.

81. (New) The method of claim 65, wherein the first or second mounted tissue is pretreated with an enzyme or a chemical.

82. (New) The method of claim 81, wherein the enzyme pre-treatment is performed with a protease, a polysaccharase, a ribonuclease, a nuclease or a combination thereof.

83. (New) The method of claim 65, wherein the tissue is bone marrow cells, lymph cells, sperm cells or cells from cerebrospinal fluid.

84. (New) The method of claim 65, wherein the initial library is a combinatorial library.

85. (New) The method of claim 84, wherein the combinatorial library is a naive antibody library, a synthetic antibody library, a semi-synthetic antibody library, or a combinatorial library produced by immunizing against one or more target structures.

86. (New) The method of claim 65, wherein step (D) of claim 1 comprises amplifying the bound or unbound elements using bacterial cells, PCR synthesis or chemical synthesis.

87. (New) The method of claim 65, wherein the monoclonal antibody or scFv/Fab fragments thereof of the initial library further comprises antibody identifying sequence information.

88. (New) The method of claim 87, wherein the sequence-identifying information is a nucleic acid or a amino acid sequence.

89. (New) The method of claim 87, wherein the sequence identifying information is in a filamentous phage or a virus.

90. (New) The method of claim 89, wherein the filamentous phage is M13.

91. (New) The method of claim 65, wherein the recovered bound element of steps (C) and (I) comprise a phage and maintain amplification ability.

92. (New) The method of claim 65, wherein the cleavage occurs between minor coat protein pIII and the monoclonal antibody or scFV/Fab fragment thereof.

93. (New) The method of claim 65, wherein the cleavage is a proteolytic cleavage and occurs at a protease recognition site.

94. (New) The method of claim 93, wherein the cleavage is a proteolytic cleavage and the protease is Ala64-subtilisin or blood clotting factor Xa.

95. (New) The method of claim 65, wherein the elution is a chemical elution.

96. (New) The method of claim 95, wherein the chemical elution is an acid or alkaline elution.

97. (New) The method of claim 96, wherein the alkaline elution is triethylamine.